ME

From:

Myers, Carla

Sent:

Wednesday, October 12, 2005 7:00 AM

To: Subject: STIC-Biotech/ChemLib sequence search 09/887941

Please do an oligomer search in commercial and interference files for fragments of SEQ ID NO: **11 and 12** - please limit the search results to nucleic acids of a length of 50 nucleotides or less.

Please provide a printout of the first 40 results.

The CRF has been entered; http://expoweb1:8001/cgi-bin/expo/BioInfo/bioquery.pl?APPL_ID=09887941

Thank you

Carla Myers AU 1634 Remsen Bldg / Rm 2E79 Mailbox: REM 2C70 571-272-0747

OCT 12 2000

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Type of Search
NA# _____ AA#:
S/L: ____ Oligomer: _____
Encode/Transl: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN:_____
DIALOG:____
QUESTEL/ORBIT:___
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SEQUENCE SYSTEM:
WWW/Internet:___

Other (Specify):

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AUI07206 Sugano Homo sapiens c
HRC10935, mRNA sequence.
AUI07206
AUI07206 I GI:13556727
EST.
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200
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/mol type="maNA) 606"
/db xref=""taxon: 9606"
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                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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KAT06101, mRNA sequence
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A.
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene
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Contact: Yutaka Suzuki
Department of Virology
Institute of Medical So
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Conservative 0;
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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., (
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, 1
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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LNG05636, mRNA sequence.
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ilarity 100.0%;
Conservative (
                                                                    larity 100.0%;
Conservative 0;
                                                                                                                                                       /mol type="mRNA"
/db xref="taxon:9606"
/clone="LNG05636"
/clone_lib="Sugano Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                    Score 14; DB 1; Li; pred. No. 2.7e+04; 0; Mismatches 0;
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Pred. No.
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2.7e+04;
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RESULT 5

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Perfect score:
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                                                                                                                                                                  Score
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seq length: 50
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Match
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Gapop 60.0 , Gapext 60.0
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11:
12:
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                                                                                                                                                                                                                                                                                                                'Cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*
'Cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*
'Cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*
'Cgn2_6/ptodata/2/pubpna/US109_NEW_PUB.seq:*
'Cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
'Cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
'Cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
'Cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
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'Cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
'Cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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     US-10-098-263B-17480
US-10-719-900-56424
US-10-719-900-195425
US-10-719-900-489771
US-10-719-900-955757
US-10-719-956-315460
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Sequence 56424, A
Sequence 195425,
Sequence 489771,
Sequence 955757,
Sequence 180263,
     Sequence
     315460
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RESULT 2
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US-10-843-527-17	US-10-843-527-68092	US-10-956-157-30819	US-10-956-157-19250	US-10-809-189-1125	US-10-809-189-11250	US-10-809-189-23342	US-10-719-900-88874	US-10-719-900-84384	US-10-719-900-8376	US-10-719-900-7652	US-10-719-900-76424	US-10-719-900-74731	US-10-719-900-69585	US-10-719-900-2676	US-10-719-900-2003	US-10-719-900-1537	US-10-719-900-1091	US-10-719-900-1021	US-10-719-900-71312	US-10-098-263B-244	US-10-257-158A-4	US-10-257-158A-893	US-10-177-798-	US-10-235-463-	US-10-632-342-	US-10-632-342-19	US-11-036-317-97118	US-11-036-317-95736	US-11-036-317-93953	US-11-036-317-	US-11-036-317-89091	US-11-036-317-45273	US-11-036-317-36382	US-11-036-317-33964	US-11-036-317-30816	US-11-036-317-25796	US-11-036-317-20298
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PRIOR APPLICATION NUMBER: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 17480
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-17480
                                                                                                                                                                                                                                                                                                                                                                                                     US-10-098-263B-17480
                                                                Matches
                                                                                                                                                                                                                                                                                                     Sequence 17480, Application US/10098263B Publication No. US20030104410A1 GENERAL INFORMATION:
APPLICANT: Mittman, Michael TITLE OF INVENTION: Human Microarray FILE REFERENCE: 3118.1
                                                                                            Query Match
                                                                               Local
               92 CAGGAACCTCAGAGA 106
w
                                                         1 Similarity 100.0%; 1
                                                                                            7.7%;
                                                                        Score 15;
Pred. No.
                                                         Mismatches
                                                                      DB 15; I
1.5e+03;
                                                                                    Length 25;
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                                                     Gaps
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RESULT 4

US-10-719-900-489771/c

; Sequence 489771, Application US/10719900

; Publication No. US20050026164A1

; GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TILE REFERENCE: 3528.1

; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 982914
; NUMBER OF SEQ ID NOS: 982914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA; ORGANISM: Mus musculus US-10-719-900-195425
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PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 56424
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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Best Local :
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TITTLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 489771 LENGTH: 25
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100.0%; Pred. No. 1.9
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Sequence 180263, Application US/10719956

publication No. US20040146910A1

GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1

CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002-11

NUMBER OF SEQ ID NOS: 699466

COMPRIADE: WIGHTERSTON NUMBER: 699466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA; ORGANISM: Mus musculus US-10-719-900-489771
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US-10-719-900-955757
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                                                                                                                                                                                        ORGANISM: Rattus norvegicus
US-10-719-956-180263
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RESULT 7
US-10-719-956-315460
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                                                                                                                                                                                                                      SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 180263
LENGTH: 25
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 955757
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TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR EILING DATE: 2002 11 20
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es 15; Conservative (
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100.0%; Pr
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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US-08-936-196G-23342
US-09-396-196G-112506
US-09-396-196G-112507
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US-09-396-196G-112507
US-09-866-108A-2615
US-09-866-108A-2616
US-09-866-108A-2619
US-09-167-109-86
US-09-167-116-26
US-09-387-341-223
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US-09-386-108A-5544
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Sequence 2619, Ap
Sequence 2619, Ap
Sequence 46, Appl
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Sequence 70, Appl
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SEQ ID NO 19
LENGTH: 19
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RESULT 2
US-09-000-630C-17/c
US-09-000-630C-17/c
; Sequence 17, Application US/09000630C
; Patent No. 6018029
; GENERAL INFORMATION:
; APPLICANT: Fuller, Gerald M
; APPLICANT: Fuentes, Nelson L.
; TITLE OF INVENTION: DNA Encoding Ca
; TITLE OF INVENTION: Antagonist
; NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 06275-165002

CURRENT APPLICATION NUMBER: US/09/422,936

CURRENT FILING DATE: 1999-10-22

PRIOR APPLICATION NUMBER: US 09/242,608

PRIOR FILING DATE: 1998-02-19

PRIOR PPLICATION NUMBER: PCT/SE98/01947

PRIOR FILING DATE: 1998-10-27

PRIOR PLING DATE: 1998-10-27

PRIOR PLING DATE: 1997-10-27

PRIOR PRIOR DATE: SWEDEN 9703914-2

PRIOR APPLICATION NUMBER: SWEDEN 9800864-2

PRIOR APPLICATION NUMBER: SWEDEN 9800864-2

PRIOR APPLICATION NUMBER: SWEDEN 9802575-2

PRIOR FILING DATE: 1998-07-17

PRIOR FILING DATE: 1998-07-17

NUMBER OF SEQ ID NOS: 85

CONTENTALE: ESTEC 66
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TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
FILE REFERENCE: 06275-165002
                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Douglas C
                                                                                                                                                                                                                                                                                                                                                                                                    118 AGGCCCGGGGAGAG 131
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3: Douglas C Murdock/ Bradley,
2001 Park Place, Suite 1400
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JMBER: SWEDEN 9802575-2
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Pred. No. 1.5e+03;
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,

35203-2736

COUNTRY:

USA

CITY: Birmingham

Alabama

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                                              Query Match 7.1%; S. Best Local Similarity 100.0%; Matches 14; Conservative 0;
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Best Local Similarity
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APPLICANT: Fuller, Gerald M
APPLICANT: Fuentes, Nelson L.
TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor
TITLE OF INVENTION: Antagonist
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 24 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: oligonucle
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                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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                                                                                                                                        LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
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109 GAGGCTGACAGGCC 122
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                                              7.1%; Score 14; DB 3; [00.0%; Pred. No. 1.5e+Cive 0; Mismatches
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TRESULT 6
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                                                                                                                                                                                                                                             ; ORGANISM: mus musculus 
US-09-396-196G-112506
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US-09-396-196G-23342/c
                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 112506
LENGTH: 25
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Patent No. 6821724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 23342
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Patent No. 6821724
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
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TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/100,678 PRIOR FILING DATE: 1998-09-17
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PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
                                                                                                                                                                                                                                                                              LENGTH: 25
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David Lockhart
                                                                                                                                                                       7.1%; Score 14; DB 4; L llarity 100.0%; Pred. No. 1.5e+03; Conservative 0; Mismatches 0;
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GENERAL INFORMATION: APPLICANT: Michael Mittmann

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   GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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Aba01159 Human zin
Aaq10273 Probe B(I
Aba01162 Human zin
Aba01161 Human zin
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Aax58088 PCR prime
Abi97219 Capture o
Adj31930 Human orp
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Aat94895 Human GAB
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RESULT 1
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ID ACIT 13-C
XX EST;
KW Gene
KW CTOS
XX HOMC
XX US2C
XX US2C
XX I6-P
PD 05-C
XX AFI
XX AFI
XX WPI;
PT Sequ
XX CC Ine
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genetic variation;
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                                                                                                                                                                                                                                                                                    cross-species comparison.
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                                                                                                                                                                                                       15-MAR-2002; 2002US-00098263
                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                       Human microarray DNA oligonucleotide SEQ ID
                                                                                                                                                                                                                                                                                                                                             13-OCT-2003
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                                                                                                                                                                                                                                                                                           expressed sequence tag; microarray; gene expression;
on; biallelic marker; polymorphism; human;
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis Claim 1; New array of nucleic acid probes, useful for Southern, Northern or dot-blot hybridization sequence or specific mutations of any gene. SEQ ID NO 17480; 9pp; English. 0 11 situ hybridization, in identify or detect the

WPI; 2003-567953/53.

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RESULT 2
ABA01159
ID ABA0
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                                The present invention relates to human zinc finger protein 72 (see AAM52332). The zinc finger protein and its coding sequence are useful the diagnosis and treatment of cancer, haemopathy, HIV infection, immunological diseases, various inflammations, nervous system diseases and developmental disorders. The present sequence is a PCR primer, whi was used in an example from the present immorting.
                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probes is useful in in situ hybridisation, in Southern, Northern or dotablot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequance.sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises at across-species comparison are found to the comprises at a contract of the nucleic acids.
                                                                                                                                                                                      Example 5;
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                                                                                                                                                                                                                                                                      New human zinc finger protein 72 for diagnosing and treating malignant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiinflammatory; haemostatic; anti-HIV; gene therapy; cancer; haemopathy; HIV infection; immunological disease; inflammation; nervous system disease; developmental disorder; PCR primer; ss.
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                        24-JAN-2002
                                                                 ABA01162;
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 38
                                                                                                          ABA01162
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03-APR-1991
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Copyright (c) 1993 - 2005 Compugen Ltd.
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AX2971/7 Sequence
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AR302009	BD247913	AX803879	AX023789	BD251425	AX955736	AX955684	AX295275	AX286799	AR559926	AR215675	CQ871039	BD265675	AR137950	CQ790275	AR156414	AR534963	AR429072	AR365580	AR211174	AR211173	BD264357	BD224952	BD224951	BD140553	AX803878
AR302009	BD247913	AX803879	AX023789	BD251425	AX955736	AX955684	AX295275	AX286799	AR559926	AR215675	CQ871039	BD265675	AR137950	CQ790275	AR156414	AR534963	AR429072	AR365580	AR211174	AR211173	BD264357	BD224952	BD224951	BD140553	AX803878
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Sequence 8939 from Patent
AX297177
AX297177.1 GI:17058868
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Patent: US 6465213-A 19 15-OCT-2002;
Cocation/Qualifiers
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Barany,F., Zirvi,M., Gerry,N.P., Favis,R. Method of designing addressable array for
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AR236573
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NEW G-PROTEIN CONJUGATED TYPE RECEPTOR PR
PATENT: JP 1997238686-A 2 16-SEP-1997;
TAKEDA CHEM IND LTD

OS NONE

OC Artificial sequences.
PN JP 1997238686-A/2
PD JF 197238686-A/2
PD JF 197238686-A/2
PD JF 197238686-B/2
PD J
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CC strandedness: Single;
CC topology: Linear;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FH Key Location/Qualifiers
FH Key 1. .24
FT source /organism='Artificial sequences'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR primer for gaining human E13893
  AX292544
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Similarity 100.0%; Pred. No. 3.1e+04;
14; Conservative 0; Mismatches 0;
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HINUMA KUNIJI, FUJII AKIRA
C12N15/09,A61K48/00,C07H21/04,C12N1/21,C12P21/02,C12P21/08,
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                                                                                                                                                                                                                                                                                                           /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"
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/mol type="unassigned DNA"
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Sequence 12 d
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AX815614.1 (
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Use of the gaba b? receptor in assays to identify gamma hydroxybutyrate agonists, antagonists, and allosteric modulators
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Sequence 13 from Patent WO0190163.
AX318212
AX318212.1 GI:17900895
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/mol_type="unassigned DNA"
/db_xref="tcaxon:32630"
/noTe="PCR primer"
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/db_xref="taxon:32630"
/note="Hypothetical Probe
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   GI:39646311
                                  from Patent WO03066904.
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AZ830331 AZ877472 AI631069 ACC178512 AJ5915261 AJ5915261 AJ591106 AZ642731 AU104712 AU104713 AU104713 AU107973 AU107973

2M0192L19 tz32b10.x NPX329 Ba NPX329 Ba 1M0198021 Arabidops KG09864-5

2M0109H03

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Gapop 60.0 , Gapext 60.
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gb_est5: *
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   CL437571
AB094450
CG722869
BH755587
AA732952
CL658678
CF310621
AZ513870
CL523870
CL5258870
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(without alignments)
4393.656 Million cell updates/sec
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CG722869 1119073G0
BH755587 SALK 0518
AJ732952 AJ732952
CL658678 PRI0132a
CF310621 ABF--05-F
AZ513870 1M0360K08
CL529376 HIV40G02
AU102598 AU107543
BX288916 Arabidops
CG7310774 3119018F0
CG737471119018F0
CG7324209 HINN--05-O
AZ454352 1M0256G18
AZ582689 1M0376D13
AU2556240 AU256240
N22525 yw45e09-81
AZ356943 1M0098D16
AZ86892 2M0105N15
                                                                                                                                                        CL529376 | AU102598 | AU107543 | BX288916 | CG710737 | CF324209 | AZ454352
                    AZ408275
BX656232
CF307411
                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
   Arabidops
HDA1--06-
SK2-0117
                                                     1M0179G20
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Matches 16; Conserv
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Class:
                                                                                                                                                                                                                                                                                                                              Email: hicksgg@cc.umanitoba.ca
U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
sequence information and target gene cloning can be generated. ES
cell line harboring insertion mutation of target gene is available.
Sequence analysis available from
http://140.193.242.7/esdb/public_search_frame.php?PST=PST5874-NL.Se
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, Universitry of Manitoba
ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
Tel: 204 787 2133
Fax: 204 787 2190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2002)
Contact: Hicks GG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 40)
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PST5874-NL.Seg MICB1 Mus genomic survey sequence.
CL437571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hicks, G.G
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Conservative 0;
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                                                                                      /cell_type="Embryonic stem cel
/cell_line="D3H (J1 subclone)"
/clone_lib="MICBI"
/note="Vector: U3NeoSV1"
                                                                                                                                                                                                            organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
                                                                                                                                                                             'clone="PST5874-NL.Seq"
                                                                                                                                                                                               db_xref="taxon:10090"
7.3%; Score 16; DB 9; Le:
100.0%; Pred. No. 2.5e+03;
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BH901106
AZ642798
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                                                                                                                                          stem cell"
                                   Length 40
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CG722869
CG722869.1 GI:3
GSS.
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                        Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA
                                                                       Maize genomic sequences
Unpublished (2001)
Contact: Walbot V
                                                                                                                                   Zea mays

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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AB094450 AB094450 AB094450 AB094450 GI:30307355
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Tel: 650 723 2227 Fax: 650 725 8221
                                                                                                                      Walbot, V.
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Kannondail-25-2, Tsukuba, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hmano@pgcdna.co.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa
/mol_type="mRNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="phloem"
/clone_lib="lambda TriplEx2 rice phloem sap cDNA"
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/clone="PA158"
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                              CA 94304, USA
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                                                                                                                                                                                                                                                                                                                                  Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
                                                                                                                                                                                                                                                                                                                                                                                                     Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., P. Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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                                                                                                                                                                                                                                                                                   Salk Institute Genomic Analysis Laboratory (SIGnAL) The Salk Institute for Biological Studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana
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Tel: 858 453 4100 x1752
Fax: 858 558 6379
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                                                                                                                  At2g38080.
                                                                                                                                        This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of
                                                                                                                                                                                       Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     survey sequence.
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/clone lib="119" - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from
/note="Organ: leaf; Vector: RescueMu (engineered from
/notesueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."
                                                                                                TDNA tagged
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
                                                                     Location/Qualifiers
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/cultivar="mixed_background_W23/A188/B73/K55"
/db_xref="taxon:4577"
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/lab_host="DH10B"
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Result
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
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                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq length: 0 seq length: 50
      Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-887-941B-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8765912 seqs, 3504951483 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapop 60.0 , Gapext 60.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO9A_PUBCOMB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO9A_PUBCOMB.seq:*
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/ Cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/US09NEW_PUB.seq:*
/ Cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10L_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
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    US-10-719-900-365536

US-10-719-900-616433

US-10-719-900-654770

US-10-719-900-717050

US-10-719-900-958924

US-11-036-317-20600

US-11-036-317-23369
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Sequence 365536,
Sequence 616433,
Sequence 654770,
Sequence 717050,
Sequence 958924,
Sequence 23600, A
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9	25	11.4	25	24	11-036-317-70907		
10	25		25	24	-11-036-317-12138	Φ	2138
11	25	۳	25	24	-11-036-317:-5956	equenc	956
12	25	11.4	25	24	-11-036-317-61066	equenc	1066
13	25	۳	25	24	-11-036-317-72102	equenc	2102
14	25	-	25	24	1-036-317-84604	equenc	46045
15	24		24	20	-10-479-306-47	equenc	7, A
16	21	9	25	21	-10-719-900-5085	quenc	08538
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18	21		25	24	-11-036-317-5433	equenc	4334,
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21	18		25	24	-11-036-317-9535	equenc	5354
22	17		25	21	-10-719-900-81072	Ф	1072
23	17	٠	25	24	-11-036-317-55915	eque	5915
24	17	٠	25	24	-11-036-317-13597	equenc	3597
25	17		25	24	-11-036-317-26194	æ	6194
26	17		25	24	-11-036-317-36073	Φ	6073
27	17		25	24	-11-036-317-77142	Φ	7142
28	17		25	24	-11-036-317-96955	Ø	6955
9	16		25	21	-10-719-900-31091	m	1091
30	16		25	21	-10-719-900-6994	Ð	994
31	16		25	21	-10-956-157-10867	equenc	0867
32	16		25	21	0-956-157-10867	equenc	0867
33	16		25	21	-10-956-157-10867	ø	0867
4	16	٠	25	2	-10-956-157-10867	equenc	0867
35	16		25	21	-10-956-157-10868	equenc	8980
8	16	•	25	21	-10-956-157-10868	Ф	8980
37	16	•	25	24	-11-036-317-322	Œ	223, A
8	16	•	25	24	-11-036-317-1394	equenc	3946
9	16	•	25	24	-11-036-317-18126	æ	8126
5	16	•	25	24	-11-036-317-24477	æ	4477
=	16		25	24	-11-036-317-510	æ	10
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ALIGNMENTS

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Sequence 365536, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
                                                                                                                                             US-10-719-900-365536
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
US-10-719-900-365536
                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982514
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 36536
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
                                                                     Matches
                                                                                                      Query Match
                                                                                       Best Local
                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/719,900 CURRENT FILING DATE: 2003-11-20
                                  155
ш
                                                                                       Similarity
                       CGTGCGACATTTCCCGAATTCTGCA 179
                                                                   11.4%; Score 25; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
                                                                     Mismatches
25
                                                                                       DB 21;
0.011;
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                                                                                                        Length 25;
                                                                         Indels
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                                                                       Gaps
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RESULT

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US-10-719-900-616433

GENERAL INFORMATION:

Sequence 616433, Application US/10719900 Publication No. US20050026164A1

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Sequence 717550, Application US/10719900

Publication No. US20050026164A1

GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou

ITITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR FILING DATE: 2002 11 20

NUMBER OF SEG ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SOFTWARE: MICROARRAY Probe Sequence Listing Generator V 1.1
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US-10-719-900-717050
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; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-616433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 98.9914
SOFTWARE: Microarray Probe Sequence Listing Generator SEQ ID NO 654770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 654770, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
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CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 616433
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TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
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; Pred. No. 0.011;
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RESULT 7

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Sequence 958924, Application US/10719900

Publication No. US20050026164A1

GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou

ITITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR FILING DATE: 2002 11 20

NUMBER OF 520 ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 958924
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US-10-719-900-958924
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                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: Williams, Alan
APPLICANT: Williams, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT FILING DATE: 2005-01-13
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
ANUMBER: OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 20600
LENGTH: 25

LENGTH: 25
                                                                                    Best
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Publication No. US20050214823A1
                                                                     Matches
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Best Local
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ORGANISM: Mus musculus
                                                                                                                                                                           TYPE: DNA
                                                                                                                                                            ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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les 25; Conserv
                        150 CCGGCCGTGCGACATTTCCCCGAATT 174
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100.0%; PI
                                                                  11.4%; Score 25; DB 24;
100.0%; Pred. No. 0.011;
tive 0; Mismatches 0
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Pred. No.
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Pred. No. 0.011;
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. 0.011;
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Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Listing first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
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Perfect score:
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score grea
and is der
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       nucleic search, using sw model
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Match
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Gapop_60.0 , Gapext 60.0
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220
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
      ctgctctcttcttctttt.....ccactcgccgcccccgcggc
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                                                                                                                                                                                                                                                                                                                                                        Length
       GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                          DB
  US-08-857-946-149
US-08-970-740-149
US-08-970-740-150
US-08-970-740-150
US-08-970-740-150
US-08-413-813-41
US-08-467-346-41
US-08-488-373-1
US-08-38-911-5
US-08-38-911-5
US-08-137-361C-17
PCT-US94-05591-5
PCT-US94-05591-5
PCT-US94-05591-17
PCT-US94-05591-17
PCT-US94-05591-17
PCT-US94-05591-17
US-09-357-073-13
US-09-357-073-13
US-09-357-073-14
US-09-396-196G-25595
US-09-396-196G-66126
US-09-396-196G-66126
US-09-396-196G-65137
US-09-396-196G-55137
US-09-253-396A-59
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3659.630 Million cell updates/sec
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Sequence 149, App
Sequence 149, App
Sequence 150, App
Sequence 150, App
Sequence 41, Appl
Sequence 41, Appl
Sequence 30, Appl
Sequence 10, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 5, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 2778, Appl
Sequence 6116, Appl
Sequence 66126, A
Sequence 66137, Appl
Sequence 6137, Appl
Sequence 6137, Appl
Sequence 614, Appl
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Best Local Similarity 100.0%; F
Conservative 0;
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-	•	Sequence 93, Appl		93,	90,	Sequence 16, Appl	93,	90,	•	90,	93,	•	93,		-	-	Sequence 93, Appl	

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; MOLECULE TYPE:
; FEATURE:
; NAME/KEY: pri
US-08-857-946-149
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Patent No. 5994075
GENERAL INFORMATION:
                                                                                                                                                              NAME: Kathleen M. Williams
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 3529/05573
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEPHAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 149:
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/017,824
FILING DATE: 17-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/857,946
FILLING DATE: 16-MAY-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02109-1807
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 38 bases
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TITLE OF INVENTION: METHODS
TITLE OF INVENTION: GENE OF
NUMBER OF SEQUENCES: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
CITY: BC
STATE: M
COUNTRY:
                                                                          TOPOLOGY:
                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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                                                      other nucleic
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9.1%; Score 20; 100.0%; Pred. No.

Mismatches

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Gaps

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Length 38; Indels

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                                                                                                            Sequence 150, Application US/08857946 Patent No. 5994075
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                                                                            GENERAL INFORMATION:
APPLICANT: Goodfe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-227-4399 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/85;
FILING DATE: 16-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION UDMBER: 60/01:
APPLICATION UDMBER: 60/01:
FILING DATE: 17-MAY-1996
ATTORNEY/AGENT INFORMATION:
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COMPOTIER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WOrdPerfect 6.1
CURRENT APPLICATION DATA:
                CORRESPONDENCE ADDRESS
                            TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 35
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-227-7111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 14-NOV-PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Goodfellow, P.N.
TITLE OF INVENTION: METHODS FOR IDENTIFYING A MUTATION IN
TITLE OF INVENTION: GENE OF INTEREST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Kathleen M. Williams
REGISTRATION NUMBER: 34,380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                            50 GTCACAGCGGAGTGAATCAG 69
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                                                                            Goodfellow, P.N.
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Banner & Witcoff,
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2N DATT
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                            METHODS FOR IDENTIFYING A MUTATION IN A GENE OF INTEREST
162
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                                                                                                                                                                                                                                                                                         9.1%; Score 20; DB 3;
100.0%; Pred. No. 2.6;
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                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                       Length 38;
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US-08-970-740-150/c
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US-08-857-946-150
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION: APPLICANT: Goodfe
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INFORMATION FOR SEQ ID NO:
               FILING DATE: 14-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/857,946
FILING DATE: 16-MAY-1997
PRIOR APPLICATION DATA:
                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,74
                                                                                                                                                                             ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/6:
PILING DATE: 17-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 16-MAY-1997
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: other nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                              STREET: L. Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 6.1
 APPLICATION NUMBER:
                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 3529/05573
                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Kathleen M. Williams REGISTRATION NUMBER: 34,38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 GACATTTCCCGAATTCTGCA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 GACATTTCCCGAATTCTGCA 21
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28 State Street, 28th Floor
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60/017,824
                                                                                                US/08/970,740
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Perfect score:
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seq length: 50
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Query
Match
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220
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11:
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13:
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GenCore version 5.1.6 (c) 1993 - 2005 Compu
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AAT42888
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        ABN86446
AAV82770
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Million cell updates/sec
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      Adt76402 Nucleotid
Add76402 Nucleotid
Abn86446 II-1beta
Aav82770 Double st
Aad39253 Platelet
Aad79596 Primer #2
Aad79899 Primer to
Aad79089 Primer to
Aad27012 Human end
Aaa27012 Beta-lact
Add19487 Salmo sal
                                                                                     Abz80324 Human Pax
Adg07907 Sense pri
Aav16077 PCR prime
Aaz43408 Murine c-
Aaa05393 PCR prime
Aav16078 PCR prime
Aav43409 Murine c-
Aaa05394 PCR prime
Adg76401 Nucleotid
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6 II-lbeta
6 Double st
7 Platelet
7 Primer #2
8 Primer to
9 Primer to
9 Human end
2 Beta-lact
17 Salmo sal
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45	44		42	41	40		c 38		36	35	c 34	c 33	32	c 31	c 30		c 28	27	26	25	24	23	22	21
14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	15
6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.8
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AAQ62886	AAQ30638	AAQ30641	ACC45050	AAQ49319	AAT79653	AAZ27084	ADT01047	ACI46149	ACF03717	AAZ29237	AAZ26085	AAV07765	AAV07766	ABD27463	ABD27462	ABZ91233	ABZ91232	AAZ98564	AAZ98563	AAZ98565	AAZ98562	ADE49029	AAI66200	ABZ06425
Aaq62886 GGF prime	Aaq30638 Primer 65	Aaq30641 Primer 66	Acc45050 Human PRE	Aaq49319 Degenerin	Aat79653 Oligonucl	Aaz27084 Saccharom	Adt01047 Novel mut	Aci46149 Human mic	Acf03717 PCR prime			Aav07765 Oligonucl	Aav07766 Oligonucl	Abd27463 H37989-de	Abd27462 H37989-de	Abz91233 Human oli	Abz91232 Human oli	Aaz98564 Human MAP	Aaz98563 Human MAP	Aaz98565 Human MAP	Aaz98562 Human MAP	Ade49029 Human pat	Aai66200 Peptide n	Abz06425 Human leu

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RESULT 1
ABZ80324
ID ABZ80324
ID ABZ80324
ID ABZ80324
ID ABZ8
XX ABZ8
AC ABZ8
AC ABZ8
XX Puri
KW Puri
KW PCR
XX Homc
OS Syntt
XX WPCR
YX WO2C
XX The
PT Genu
P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Purification; neural stem cell; NSC; undifferentiated; nootropic; neuroprotective; antiparkingonian; gene therapy; nervous system; central nervous system; (NS; Altheimer's disease; Parkinson's disease; acute brain injury; CNS dysfunction; tissue regeneration; tissue repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Pax6 sense PCR primer SEQ ID NO:47.
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The present invention describes a method (M) for generating a substantially homogeneous population of undifferentiated cells a biological sample (BS), which comprises subjecting BS or its

Example 10; Page 47; 90pp; English

Generating substantially homogeneous population of undifferentiated cells from sample, by disrupting tissue sample, discriminating cells in population based on size and performing cell-surface marker-discrimination.

WPI; 2003-140465/13.

₽F,

Rietze RL;

(HALL-) HALL INST MEDICAL RES WALTER & ELIZA

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RESULT 2
ADQ07907
ID ADQ0
XX ADQ0
AC ADQ0
XX Sens
XX Anti
KW Panc
XX Unid
XX Unid
XX Unid
XX Unid
XX Unid
XX Unid
XX WO20
XX Unid
XX WO20
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PD 22-J
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XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local 9
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The invention relates to a modified human hepatic cell, which is insulin-
producing. Further disclosed is an insulin-producing cell line designated
FH-B-TPN, a method of making an insulin-producing cell line, a method of
treatment of type I diabetes, a method of making insulin in-vitro, and a
vector for the expression of pancreatic duodenal homeobox gene-1 (Pdx1),
                                                                                                                                                                                                                                                                                                                           New modified human hepatic cell, which is insulin-producing, useful as medicament for treating insulin-dependent diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antidiabetic; human hepatic cell; insulin; FH-B-TPN; type 1; diabetes; pancreatic duodenal homeobox gene-1; Pdx 1; insulin-dependent; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-OCT-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (OXFO-) OXFORD BIOMEDICA UK LTD
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24; Conservative
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                                                                                                                                                                                                                                               9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for RT-PCR analysis of PAX6 gene.
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100.0%; Prr
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                                                                                                                                                                                                                                               English.
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0.089;
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RESULT 3
AAV16077
ID AAV1
XX AAV1
XX AAV1
XX AAV1
XX MAITA
KW Sing
KW PCR
XX WO97
XX YO97
XX 16-A
XX HED
XX WPI
PF 16-A
XX WPI
PF 0600
XX WPI
XX WPI
XX WPI
CC OCG
DR WPI
CC OCG
CC Plu
CC Good
CC Flu
CC Good
CC Tree
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Best Local (
                           anterior segment malformations most commonly characterised by eye development defects broadly described as aniridia. The disease is dominant. A population of male mice were treated with ENU to provide a source of mutant PAX6 and a heterozygotic F1 generation produced. F1 Pluorescent single strand conformation polymorphism (SSCP) is utilised to identify those members of the F1 population carrying PAX6 mutations. The method provides mutational screening based on genomic and genetic techniques rather than on phenotypic observation. The method identifies and characterises genes via mutagenesis to identify genes encoding products which may have therapeutic benefit. The method also identifies the presence of mutations in a gene which do not rely solely upon prior matching of a gene with a disease. Heterozygotic organisms can also be screened to identify those carrying a mutation in a copy of a gene of interest even though the gene may be recessive and therefore causes no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primers AAV16059-76 were used to identify PAX6 mutations in mice using the method of the invention. The method comprises testing a nuclei acid sample from a mutated organism for a mutation in a gene of interest without the prior observation of a phenotypic alteration in the mutated organism resulting from the mutation. PAX6 mutations lead to a variety of the mutation.
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RESULT 2 LOCUS DEFINITION ACCESSION ERSION ERSION ERSION CEYWORDS SOURCE ORGANISM	Query Match Best Local Matches 2 Matches 50 Db 19	SOURCE ORGANISM ORGANISM CORGANISM CORGINAL SOURCE	A67657 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS
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Methods for identifying a mutation in a phenotypic guide
phenotypic guide
Patent: US 5994075-A 150 30-NOV-1999;
Location/Qualifiers
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Goodfellow, P.N.
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Patent: US 5994075-A 149 30-NOV-1999;
Location/Qualifiers
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                                        /organism="unknown"
/mol_type="unassigned DNA"
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/db_xref="taxon:32644"
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/mol_type="unassigned
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Patent: US 5872105-A 41 16-FEB-1999;
Location/Qualifiers
                                                                                                                                                                                           Unknown.
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Sequence 41 from patent
AR036378
                                                                                                                                                                                                                                                                                                                                                                        16;
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Takagi,M., Shinji.H. and Ota,K.
Peptide having a function regulating t
Patent: JP 2001292776-A 2 23-OCT-2001;
AGENCY OF IND SCIENCE & TECHNOL
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MASARU TAKAGI,HIDEAKI SHINJI,KEN OTA
C12N15/09,C07K14/415,C12N5/10//(C12N15/09,C12R1:91),C12N15/00,
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JP 2001292776-A/2
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                                                                                /organism="unknown"
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                                     100.0%;
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